

X-15648.ST25.txt
SEQUENCE LISTING

<110> Beals, John
Kuchibhotla, Uma

<120> HETEROLOGOUS G-CSF FUSION PROTEINS

<130> X-15648

<150> PCT/US03/03120
<151> 2003-02-21

<160> 66

<170> PatentIn version 3.2

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X-15648.ST25.txt

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| cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ctttctaggt cccgctaccg | 180 |
| cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctgggtg | 240 |
| ctcttcgaca cattgtgggt gttcgacacg gtggggctcc tcgaccacct gctcggacac | 300 |
| tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agaccgtag | 360 |
| gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc | 420 |
| caactccata gcgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg | 480 |
| ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag | 540 |
| atgggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttggac | 600 |
| acactgcagc tggacgtcgc cgacgggctc aaccacgggt ggaacctgtg tgacgtcgac | 660 |
| ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct | 720 |
| aaacgggtggg ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc | 780 |
| accacgggtg ccatgccggc cttcaactct accttccggg acgtcgggtg ggtcccacgg | 840 |
| tacggccgga agttgagatg gaagcagcgc cgggcaggag gggtcctggg tgcctcccat | 900 |
| ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag | 960 |
| ctggaggtgt cgtaccgcgt ctttaaggcac cttgcccagc ccgacctcca cagcatggcg | 1020 |
| cagaattccg tggaacgggt cggg | 1044 |

<210> 12
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | |
|---|-----|
| <400> 12 acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg | 60 |
| ggacggtcga gggacgggggt ctcgaaggac gagttcgctt tagagcaagt gaggaagatc | 120 |
| cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ctttctaggt cccgctaccg | 180 |

X-15648.ST25.txt

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| cgctcgcgagg | tcgagaagct | gtgtaacacc | accaagctgt | gccaccccga | ggagctggtg | 240 |
| ctcttcgaca | cattgtggtg | gttcgacacg | gtggggctcc | tcgaccacct | gctcggacac | 300 |
| tctctgggca | tcgttaacgc | taccctgagc | agctgcgacg | agcctgtgac | agacccgtag | 360 |
| caattgcat | gggactcgtc | gacgcccagc | caggccctgc | agctggcagg | ctgcttgagc | 420 |
| caactccata | gcgggtcggg | ccgggacgtc | gaccgtccga | cgaactcggg | tgaggtatcg | 480 |
| ggccttttcc | tctaccaggg | gctcctgcag | gccctggaag | ggatctcccc | ggaaaaggag | 540 |
| atggtccccg | aggacgtccg | ggaccttccc | tagaggcccc | agttgggtcc | caccttggtg | 600 |
| acactgcagc | tggacgtcgc | cgacgggctc | aaccacgggt | ggaacctgtg | tgacgtcgac | 660 |
| ctgcagcggc | tgtttgccac | caccatctgg | cagcagatgg | aagaactggg | aatggcccct | 720 |
| aaacgggtgg | ggtagaccgt | cgtctacctt | cttgaccctt | accggggagc | cctgcagccc | 780 |
| accacgggtg | ccatgccggc | cttcgcctct | gctttccggg | acgtcgggtg | ggtcccacgg | 840 |
| tacggccgga | agcggagacg | aaagcagcgc | cgggcaggag | gggtcctggt | tgctcccat | 900 |
| ctgcagagct | tcgtcgcggc | ccgtcctccc | caggaccaac | ggagggtaga | cgtctcgaag | 960 |
| ctggaggtgt | cgtaccgcgt | cttaaggcac | cttgcccagc | ccgacctcca | cagcatggcg | 1020 |
| cagaattccg | tggaacgggt | cggg | | | | 1044 |

<210> 13
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| <400> 13 | | | | | | |
| acccccctgg | gccctgccag | ctccctgccc | cagagcttcc | tgctcaagt | gggggacccg | 60 |
| ggacggctcga | gggacggggg | ctcgaaggac | gagttcgctt | tagagcaagt | gaggaagatc | 120 |
| cagggcgatg | gcgcagcgct | ccagcggaat | ctcgttcact | ccttctaggt | cccgtaccg | 180 |
| cgctcgcgagg | tcgagaagct | gtgtaacacc | accaagctgt | gccaccccga | ggagctggtg | 240 |
| ctcttcgaca | cattgtggtg | gttcgacacg | gtggggctcc | tcgaccacct | gctcggacac | 300 |
| tctctgggca | tcccctgggc | tcccctgagc | agctgcgacg | agcctgtgac | agacccgtag | 360 |
| gggacccgag | gggactcgtc | gacgcccagc | aacgccaccc | agctggcagg | ctgcttgagc | 420 |
| caactccata | gcgggtcgtt | gcggtgggtc | gaccgtccga | cgaactcggg | tgaggtatcg | 480 |
| ggccttttcc | tctaccaggg | gctcctgcag | gccctggaag | ggatctcccc | ggaaaaggag | 540 |
| atggtccccg | aggacgtccg | ggaccttccc | tagaggcccc | agttgggtcc | caccttggtg | 600 |
| acactgcagc | tggacgtcgc | cgacgggctc | aaccacgggt | ggaacctgtg | tgacgtcgac | 660 |
| ctgcagcggc | tgtttgccac | caccatctgg | cagcagatgg | aagaactggg | aatggcccct | 720 |
| aaacgggtgg | ggtagaccgt | cgtctacctt | cttgaccctt | accggggagc | cctgcagccc | 780 |
| accacgggtg | ccatgccggc | cttcgcctct | gctttccggg | acgtcgggtg | ggtcccacgg | 840 |

X-15648.ST25.txt

| | |
|---|------|
| tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat | 900 |
| ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag | 960 |
| ctggaggtgt cgtaccgcgt cttaaaggac cttgcccagc ccgacctcca cagcatggcg | 1020 |
| cagaattccg tggaacgggt cggg | 1044 |

<210> 14
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | |
|--|------|
| <400> 14 | |
| acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg | 60 |
| ggacggtcga gggacgggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc | 120 |
| cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ctttctaggt cccgctaccg | 180 |
| cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg | 240 |
| ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac | 300 |
| tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacctgtag | 360 |
| gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc | 420 |
| caactccata gcgggtcggc ccgggacgtc gaccgtccga cgaactcggc tgaggtatcg | 480 |
| ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag | 540 |
| atggtccccg aggacgtccg ggaccttccc tagaggaacg gtaccgggtc caccttggac | 600 |
| acactgcagc tggacgtcgc cgacttgcca tggccagggt ggaacctgtg tgacgtcgac | 660 |
| ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct | 720 |
| aaacgggtgt ggtagaccgt cgtctacctt cttgaccctt accgggggagc cctgcagccc | 780 |
| acccaggggtg ccatgccggc cttcgccctt gctttccggg acgtcgggtg ggtcccacgg | 840 |
| tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat | 900 |
| ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag | 960 |
| ctggaggtgt cgtaccgcgt cttaaaggac cttgcccagc ccgacctcca cagcatggcg | 1020 |
| cagaattccg tggaacgggt cggg | 1044 |

<210> 15
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | |
|--|-----|
| <400> 15 | |
| acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg | 60 |
| ggacggtcga gggacgggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc | 120 |

X-15648.ST25.txt

| | |
|---|------|
| cagggcgatg ggcgagcgct ccagcggaat ctcgttctact ccttctaggt cccgctaccg | 180 |
| cgtcgcgagg tgcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg | 240 |
| ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac | 300 |
| tctctgggca tcgttaacgc taccctgagc agctgcgacg agcctgtgac agaccgtag | 360 |
| caattgcgat gggactcgtc gacgcccagc aacgccaccc agctggcagg ctgcttgagc | 420 |
| caactccata gcgggtcgtt gcgggtgggtc gaccgtccga cgaactcggg tgaggtatcg | 480 |
| ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag | 540 |
| atggtccccg aggacgtccg ggaccttccc tagaggcccc agttgggtcc caccttgagc | 600 |
| acactgcagc tggacgtcgc cgacgggctc aaccagggtt ggaacctgtg tgacgtcgac | 660 |
| ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct | 720 |
| aaacgggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc | 780 |
| acccagggtg ccatgccggc cttgcctctt gctttccggg acgtcgggtg ggtcccacgg | 840 |
| tacggccgga agcggagacg aaagcagcgc cgggcaggag gggctcctggt tgcctcccat | 900 |
| ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag | 960 |
| ctggagggtgt cgtaccgctt ctttaaggcac cttgcccagc ccgacctcca cagcatggcg | 1020 |
| cagaattccg tggaacgggt cggg | 1044 |

<210> 16
 <211> 1044
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | |
|--|-----|
| <400> 16 | |
| acccccctgg gccctgccag ctccctgccc cagagcttcc tgctcaagtg gggggacccg | 60 |
| ggacggctga gggacgggggt ctcgaaggac gagttcgcct tagagcaagt gaggaagatc | 120 |
| cagggcgatg ggcgagcgct ccagcggaat ctcgttctact ccttctaggt cccgctaccg | 180 |
| cgtcgcgagg tgcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg | 240 |
| ctcttcgaca cattgtggtg gttcgacacg gtggggctcc tcgaccacct gctcggacac | 300 |
| tctctgggca tcccctgggc tcccctgagc aattgcgacg agcctgtgac agaccgtag | 360 |
| gggacccgag gggactcgtt aacgaccagc caggccctgc agctggcagg ctgcttgagc | 420 |
| caactccata gctgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg | 480 |
| ggccttttcc tctaccaggg gctcctgcag gccctgaacg ggacctcccc ggaaaaggag | 540 |
| atggtccccg aggacgtccg ggacttgccc tggaggcccc agttgggtcc caccttgagc | 600 |
| acactgcagc tggacgtcgc cgacgggctc aaccagggtt ggaacctgtg tgacgtcgac | 660 |
| ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct | 720 |
| aaacgggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc | 780 |

X-15648.ST25.txt

| | |
|---|------|
| accaggggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg | 840 |
| tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggt tgcctcccat | 900 |
| ctgcagagct tcgtcgcggc ccgtcctccc caggaccaac ggagggtaga cgtctcgaag | 960 |
| ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg | 1020 |
| cagaattccg tggaacgggt cggg | 1044 |

<210> 17
 <211> 1762
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic construct

| | |
|--|------|
| <400> 17 | |
| gatgcgcaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa | 60 |
| gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta | 120 |
| aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa | 180 |
| aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt | 240 |
| cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa | 300 |
| tgcttcttgc aacacaaaaga tgacaacca aacctcccc gattggtgag accagagggt | 360 |
| gatgtgatgt gcaactgctt tcatgacaat gaagagacat ttttgaaaaa atacttatat | 420 |
| gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg | 480 |
| tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca | 540 |
| aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt | 600 |
| gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc | 660 |
| cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa | 720 |
| gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt | 780 |
| gccaaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa | 840 |
| aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaaatgatga gatgcctgct | 900 |
| gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct | 960 |
| gaggcaaagg atgtcttctt gggcatgttt ttgtatgaat atgcaagaag gcatcctgat | 1020 |
| tactctgtcg tgctgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc | 1080 |
| tgtgccgctg cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt | 1140 |
| gtggaagagc ctcagaattt aatcaaacaa aattgtgagc tttttgagca gcttggagag | 1200 |
| tacaaattcc agaatgcgct attagttcgt tacaccaaga aagtaccca agtgtcaact | 1260 |
| ccaactcttg tagaggcttc aagaaacctg ggaaaagtgg gcagcaaata ttgtaaacat | 1320 |
| cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggctct gaaccagtta | 1380 |
| tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaagtctg cacagaatcc | 1440 |

X-15648.ST25.txt

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa 1500
gagttttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag 1560
agacaaatca agaaacaaac tgcacttggt gagctcgtga aacacaagcc caaggcaaca 1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag 1680
gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttggtgc tgcaagtcaa 1740
gctgccttag gcttataatg ac 1762

<210> 18
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 18

Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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Ala Pro Glu Lys Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Lys Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 19
 <211> 229
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 19

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 20
<211> 585
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 20

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

X-15648.ST25.txt

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Asn Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

X-15648.ST25.txt

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 21
<211> 703
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 21
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gggggaccgt cagtcttcct cttccccca aaaccaagg acaccctcat gatctcccgg 120
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgacgg ctccttcttc ctctatagca agctcaccgt ggacaagagc 600

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aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaagtat agt 703

<210> 22
<211> 981
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 22
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acagccgccc tgggctgcct ggtcaaggac tacttccccg aaccgggtgac ggtgtcgtgg 120
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 180
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac 240
acctgcaacg tagatcaca gcccagcaac accaagggtgg acaagagagt tgagtccaaa 300
tatggtcccc catgccacc ctgcccagca cctgagttcc tgggggggacc atcagtcttc 360
ctgttcccc caaaacccaa ggacactctc atgatctccc ggaccctga ggtcacgtgc 420
gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc 480
gtggaggtgc ataattgcaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt 540
gtggtcagcg tcctcaccgt cctgcaccag gactggctga acggcaagga gtacaagtgc 600
aaggtctcca acaaaggcct ccgctcctcc atcgagaaaa ccatctcaa agccaaaggg 660
cagccccgag agccacaggt gtacaccctg ccccatccc aggaggagat gaccaagaac 720
caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780
gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 840
ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggaggggaat 900
gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc 960
tccctgtctc tgggtaaatg a 981

<210> 23
<211> 406
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 23

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45
 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140
 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160
 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Pro
 165 170 175
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 180 185 190
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 195 200 205
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 210 215 220
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 225 230 235 240
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 245 250 255
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 260 265 270
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 275 280 285
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 290 295 300

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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
305 310 315 320

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
325 330 335

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
340 345 350

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
355 360 365

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
370 375 380

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
385 390 395 400

Ser Leu Ser Pro Gly Lys
405

<210> 24
<211> 403
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 24

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140
 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160
 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Ser
 165 170 175
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly
 180 185 190
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 195 200 205
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
 210 215 220
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 225 230 235 240
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
 245 250 255
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 260 265 270
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 275 280 285
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 290 295 300
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
 305 310 315 320
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 325 330 335
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 340 345 350
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
 355 360 365
 Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
 370 375 380
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 385 390 395 400

Leu Gly Lys

<210> 25
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic construct

<400> 25

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
 1 5 10 15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 50 55 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 130 135 140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Gly
 165 170 175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ala His
 180 185 190

Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe
 195 200 205

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Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro
 210 215 220
 Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys
 225 230 235 240
 Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His
 245 250 255
 Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr
 260 265 270
 Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn
 275 280 285
 Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu
 290 295 300
 Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu
 305 310 315 320
 Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro
 325 330 335
 Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala
 340 345 350
 Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu
 355 360 365
 Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys
 370 375 380
 Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe
 385 390 395 400
 Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu
 405 410 415
 Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr
 420 425 430
 Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp
 435 440 445
 Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu
 450 455 460
 Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala
 465 470 475 480

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Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala
485 490 495

Asp Phe Val Glu
500

<210> 26
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 26
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atgaagctg 69

<210> 27
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 27
ggggcagggg gctggctggg cccagtggag tggcttcctg cactgtccag agtgactgt 60
g 61

<210> 28
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 28
ggacagtga ggaagccact ccactgggcc cagccagctc cctgccccag agcttcctg 59

<210> 29
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 29
gaacctcgag gatcctcatt agggctgggc aagggtgcctt aagacgcggt acgacacctc 60
caggaagctc tg 72

<210> 30
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 30
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atgaagctg 69

<210> 31
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 31
gctctaaggc cttgagcagg aagctctggg gcagggagct cgctgggccc agtggag 57

<210> 32
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 32
gggcccagcg agctccctgc cccagagctt cctgctcaag gccttagagc aag 53

<210> 33
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 33
gaacctcgag gatcctcatt agggctgggc aagggtgcctt aagacgcggt acgacacctc 60
caggaagctc tg 72

<210> 34
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 34
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60
atgaagctg 69

<210> 35
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

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<400> 35
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g 61

<210> 36
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 36
ggcgcagcgc tccaggagaa gctgtgtaac accaccaagc tgtgccaccc cgaggaacta 60
gtgctg 66

<210> 37
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 37
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caggaagctc tg 72

<210> 38
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
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<400> 38
gtaagcttgc gtcgacgcta gcggcgcgcc gccatggccg gacctgccac ccagagcccc 60
atgaagctg 69

<210> 39
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 39
gcccggcgct ggaaagcgct ggcgaaggcc ggcattggcg tctggttggg ctgcagggca 60
g 61

<210> 40
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

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<400> 40
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<210> 41
<211> 72
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<220>
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<400> 41
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caggaagctc tg 72

<210> 42
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 42
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atgaagctg 69

<210> 43
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
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<400> 43
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ggggccat 68

<210> 44
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 44
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ccagcgccgg gcag 74

<210> 45
<211> 72
<212> DNA
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<220>

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<223> synthetic construct
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caggaagctc tg 72

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct
<400> 46
gctagcggcg cgccaccatg 20

<210> 47
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct
<400> 47
gctcagggtg gcgttaacga tgcccagaga gtg 33

<210> 48
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<210> 49
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<220>
<223> synthetic construct
<400> 49
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<210> 50
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
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<400> 50
gctagcggcg cgccaccatg gccggacctg ccacccag 38

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<210> 51
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 51
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 <210> 52
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic construct

 <400> 52
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 <210> 53
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic construct

 <400> 53
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 <210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic construct

 <400> 54
 gctagcggcg cgccaccatg 20

 <210> 55
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 55
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 <210> 56
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<400> 56
gctaacctga ctagttggcc cagccag 27

<210> 57
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 57
gactcgagga tcctcattag ggctggg 27

<210> 58
<211> 20
<212> DNA
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<220>
<223> synthetic construct

<400> 58
gctagcggcg cgccaccatg 20

<210> 59
<211> 25
<212> DNA
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<220>
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<400> 59
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<210> 60
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<220>
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<400> 60
gcaattgcac cagccaggcc ctg 23

<210> 61
<211> 27
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<220>
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<400> 61
gactcgagga tcctcattag ggctggg 27

<210> 62
<211> 38
<212> DNA
<213> Artificial Sequence


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<220>
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<400> 62
gctagcggcg cgccaccatg gccggacctg ccacccag 38

<210> 63
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
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<400> 63
ccggactggt cccgttcagg gcctgcagga gcccctg 37

<210> 64
<211> 35
<212> DNA
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<220>
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<400> 64
gaacgggacc agtccggagt tgggtccac ctggtg 35

<210> 65
<211> 47
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<213> Artificial Sequence

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<400> 65
gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg 47

<210> 66
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 66
gtcgacgcta gcggcgcgcc accatggccg gacctg 36

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